FIG. 1-1

Human Basic Fibroblast Growth Factor

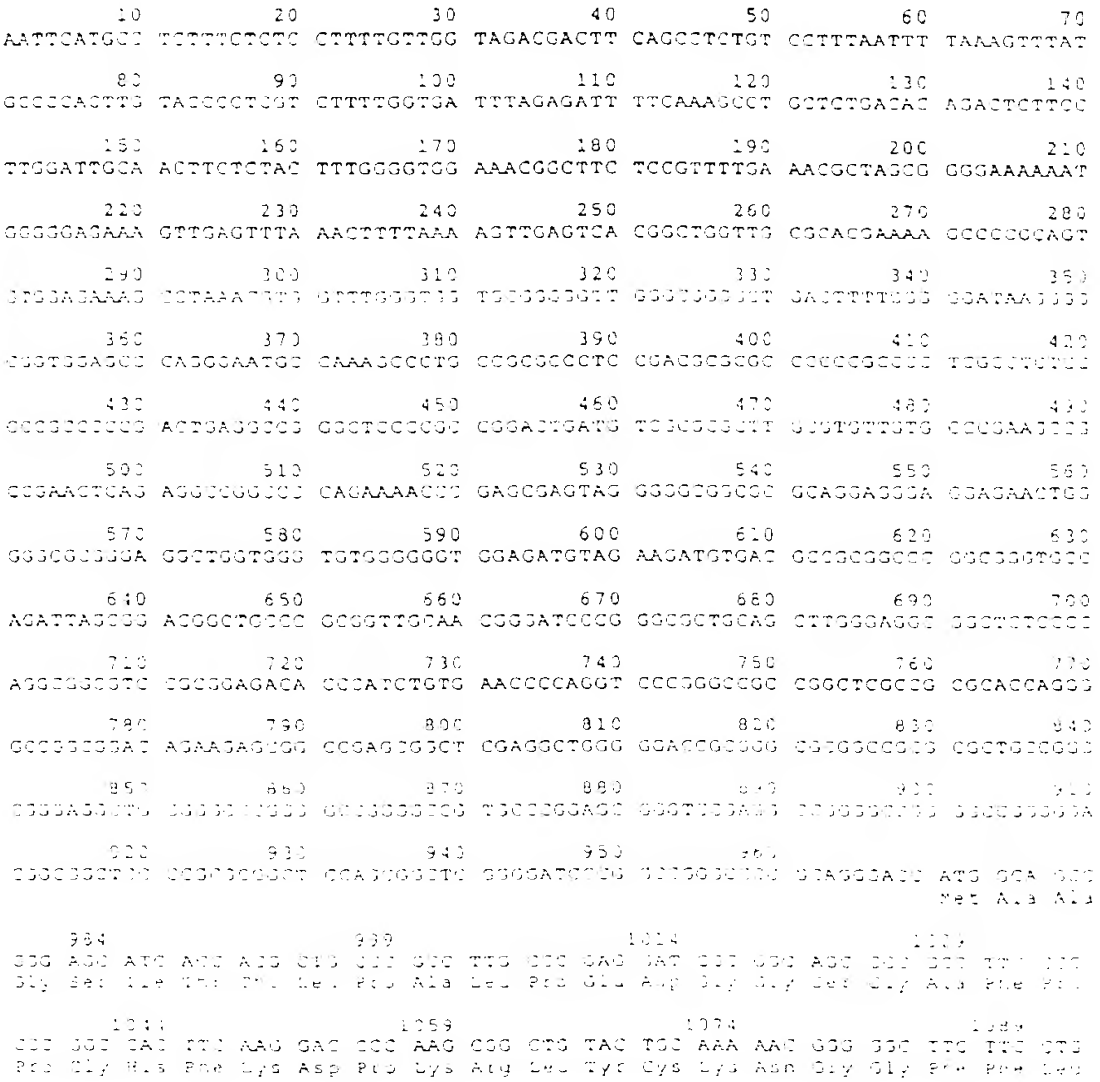


FIG. 1-2

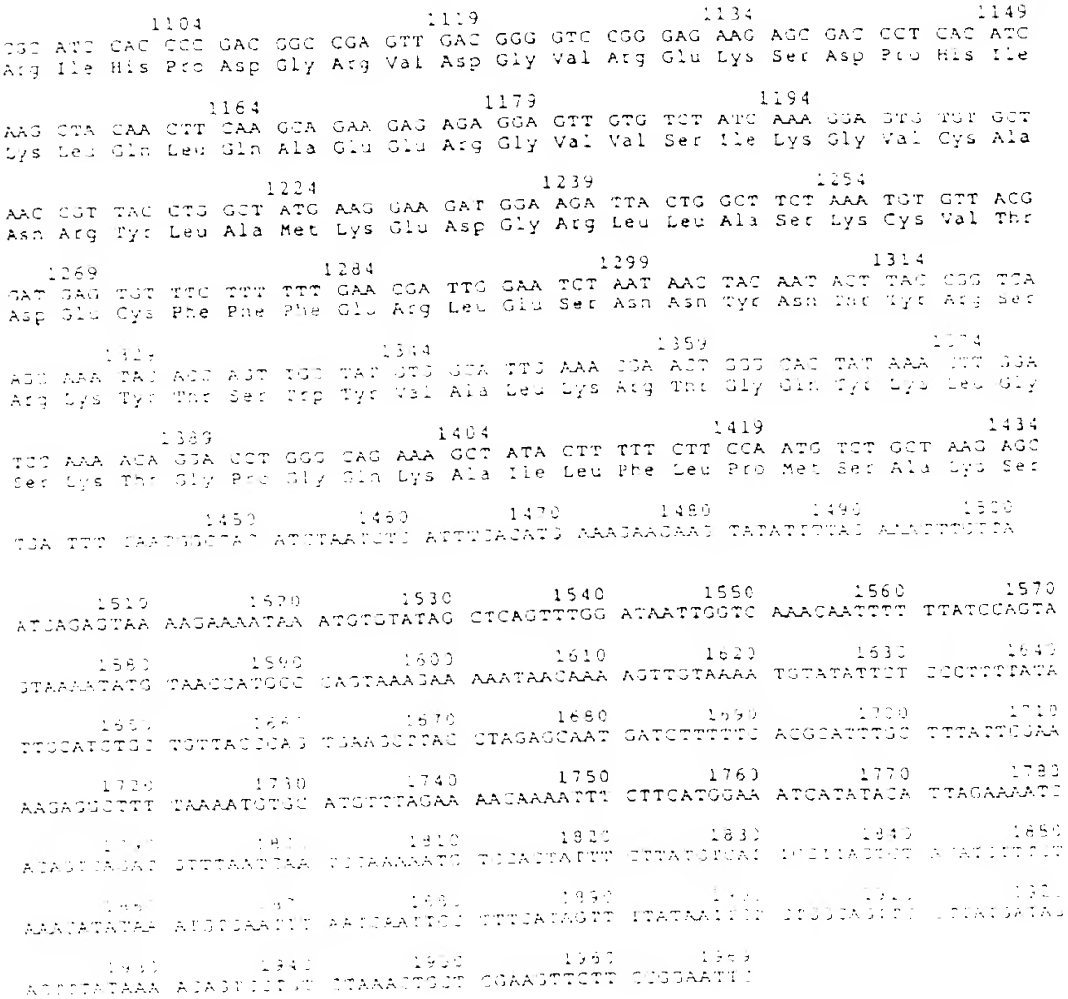

1104 1119 1134 1149
CGC ATC CAC CCC GAC GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC
Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile
1164 1179 1194
AAG CTA CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT GCT
Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala
1224 1239 1254
AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT AAA TGT GTT ACG
Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr
1269 1284 1299 1314
GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT AAC TAC AAT ACT TAC CGG TCA
Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser
1329 1344 1359 1374
AGG AAA TAC ACC AGT TGG TAT GTG GCA TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA
Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly
1389 1404 1419 1434
TCC AAA ACA GGA CCT GGG CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC
Ser Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
1450 1460 1470 1480 1490 1500
TGA TTT TAATGGCTAT ATGTAAATGTG ATTTTGACATG AAAGAACAAG TATATTGTAG AAAATTGTTA
1510 1520 1530 1540 1550 1560 1570
ATGAGAGTAA AAGAAAATAA ATGTGTATAG CTCAGTTTGG ATAATTGGTC AAACAATTTT TTATCCAGTA
1580 1590 1600 1610 1620 1630 1640
GTAAAATATG TAAGCATGGC GAGTAAAGAA AAATAACAAA AGTTGTAAAA TGTATATTGT GGCTTTTATA
1650 1660 1670 1680 1690 1700 1710
TTGCATGTGT TGTTAGGGAG TGAAGCTTAG GTAGAGCAAT GATCTTTTTG ACGCATTTGC TTTATTGGAA
1720 1730 1740 1750 1760 1770 1780
AAGAGGCTTT TAAAATGTGC ATGTTTAGAA AACAAAATTT CTTCATGGAA ATCATATACA TTAGAAAATG
1790 1800 1810 1820 1830 1840 1850
ATAGTGAGAT GTTTAATGAA TGTAAAAATG TGGACTATTT GTTATGTGAT GTGTTAGGGT ATATGTTTGT
1860 1870 1880 1890 1900 1910 1920
AAATATATAA ATGTGAATTT AATGAATTGC TTTGATAGTT TTATAATTTG GTGGGATGTG TTTATGATAG
1930 1940 1950 1960 1970
ACTGTATAAA AGAGTGGTGT GTAAATTGGT GGAAGTTGTT GGGAATTG

FIG. 2

Human Acidic FGF

27 54
TGC ATT TTG TGC CTT TGC TGG AAG AAC CGA CTA CAG CTT TGT TCA ATT TCT TAC

81 108
AGT CTT GAA AGC GCC ACA AGC AGC AGC TGC TGA GCC ATG GCT GAA GGG GAA ATC
MET Ala Glu Gly Glu Ile
1

135 162
ACC ACC TTC ACA GCC CTG ACC GAG AAG TTT AAT CTG CCT CCA GGG AAT TAC AAG
Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys
10 20

189 216
AAG CCC AAA CTC CTC TAC TGT AGC AAC GGG GGC CAC TTC CTG AGG ATC CTT CCG
Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro
30 40

243 270
GAT GGC ACA GTG GAT GGG ACA AGG GAC AGG AGC GAC CAG CAC ATT CAG CTG CAG
Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
50 60

297 324
CTC AGT GCG GAA AGC GTG GGG GAG GTG TAT ATA AAG AGT ACC GAG ACT GGC CAG
Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
70

351 378
TAC TTG GCC ATG GAC ACC GAC GGG CTT TTA TAC GGC TCA CAG ACA CCA AAT GAG
Tyr Leu Ala MET Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
80 90

405 432
GAA TGT TTG TTC CTG GAA AGG CTG GAG GAG AAC CAT TAC AAC ACC TAT ATA TCC
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser
100 110

459 486
AAG AAG CAT GCA GAG AAG AAT TGG TTT GTT GGC CTC AAG AAG AAT GGG AGC T[illegible]
Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys
120 130

513 540
AAA CGT GGT CCT CGG ACT CAC TAT GGC CAG AAA GCA ATC TTG TTT [illegible] [illegible] [illegible]
Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu
140 [illegible]

567 [illegible]
CCA GTC TCT TCT GAT TAA AGA GAT CTG TTC [illegible]
Pro Val Ser Ser Asp
155

621
[illegible]

Comparison of amino acid sequence of
human basic and acidic FGF

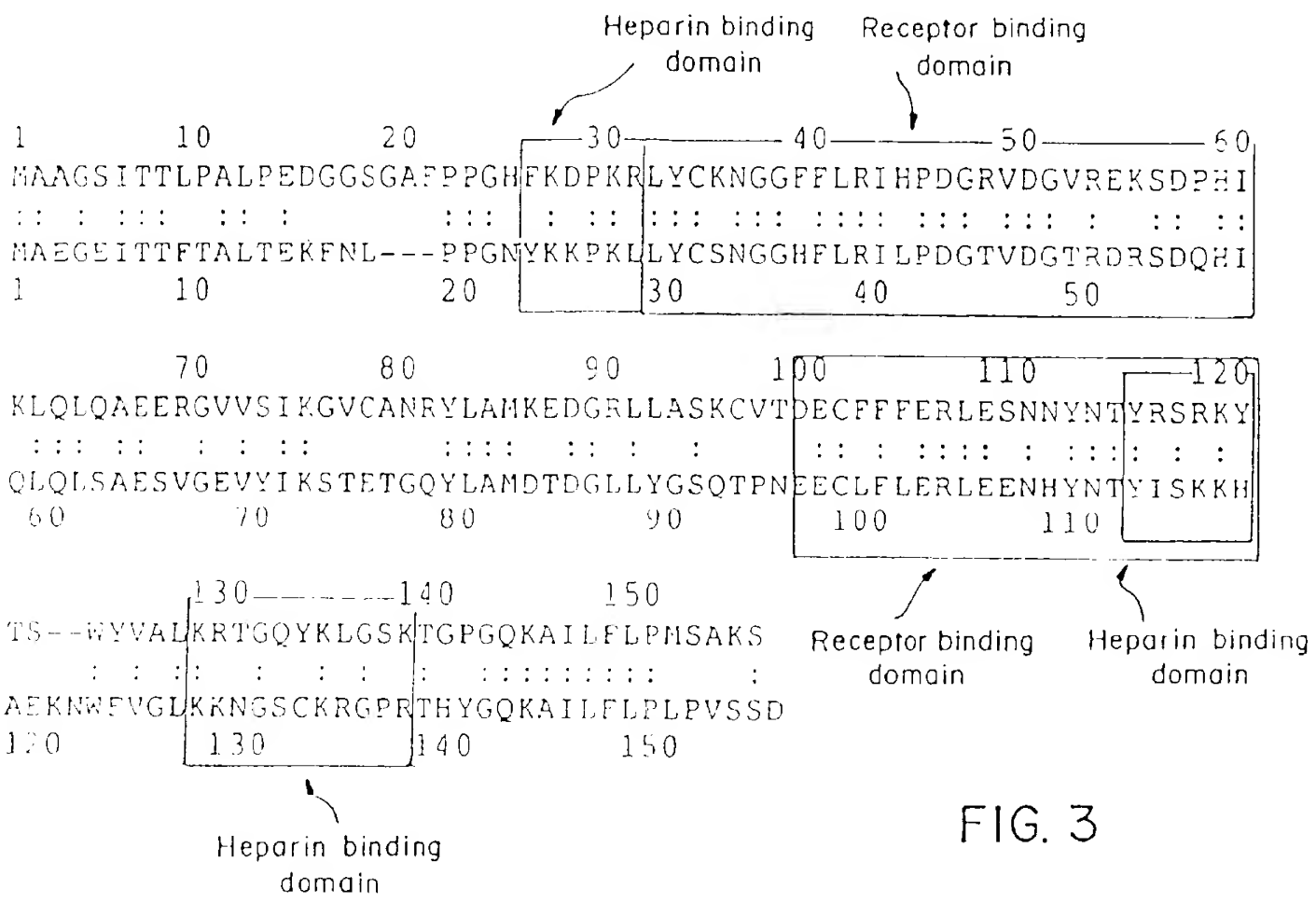


FIG. 3

APPL[illegible]ING DATE: JULY 9, 2001
TITLE: [illegible]UMAN BASIC FIBROBLAST GROWTH FACTO[illegible]ALOG
INVENTOR(S): JOHN C. FIDDES, ET AL.
APPLICATION SERIAL NO: 09/902,460

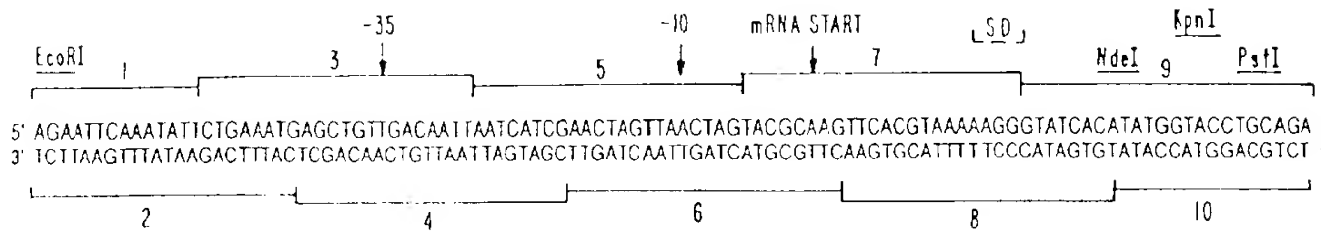
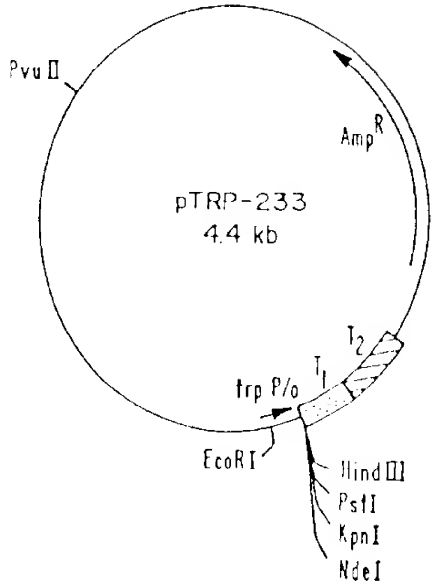
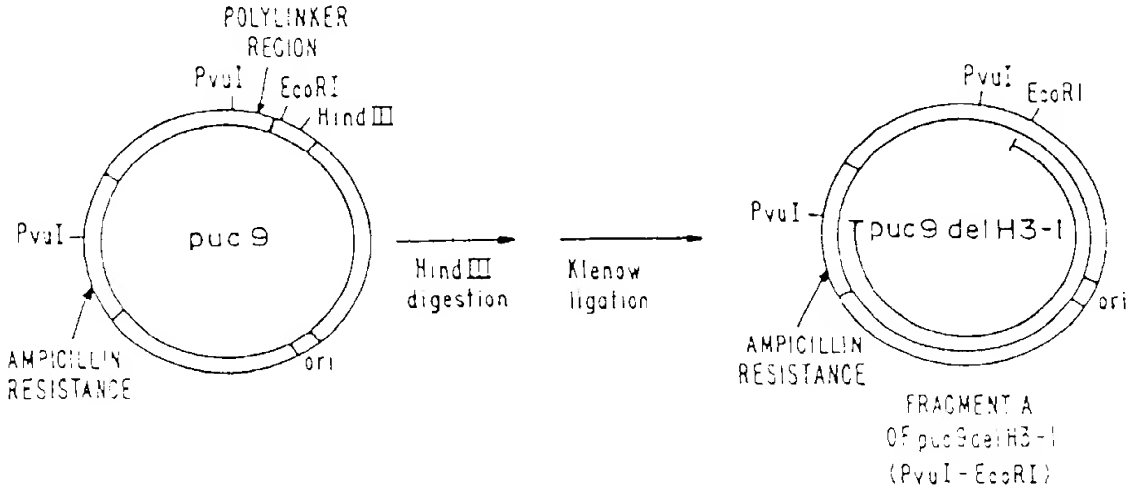

EcoRI
-35
-10
mRNA START
S.D.
KpnI
NdeI
PstI
1
3
5
7
9
5' AGAATTCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGAACTAGTTAACTAGTACGCAAGTTCACGTAAAAAGGGTATCACATATGGTACCTGCAGA 3'
3' TCTTAAGTTTATAAGACTTTACTCGACAACTGTTAATTAGTAGCTTGATCAATTGATCATGCGTTCAAGTGCATTTTTCCCATAGTGTATACCATGGACGTCT 5'
2
4
6
8
10

FIG. 4


PvuII
AmpR
pTRP-233
4.4 kb
T2
T1
trp P/o
EcoRI
HindIII
PstI
KpnI
NdeI


POLYLINKER REGION
PvuI
EcoRI
HindIII
PvuI
puc 9
AMPICILLIN RESISTANCE
ori
HindIII digestion
Klenow ligation
PvuI
EcoRI
PvuI
Tpuc9 delH3-1
ori
AMPICILLIN RESISTANCE
FRAGMENT A OF puc9delH3-1 (PvuI-EcoRI)

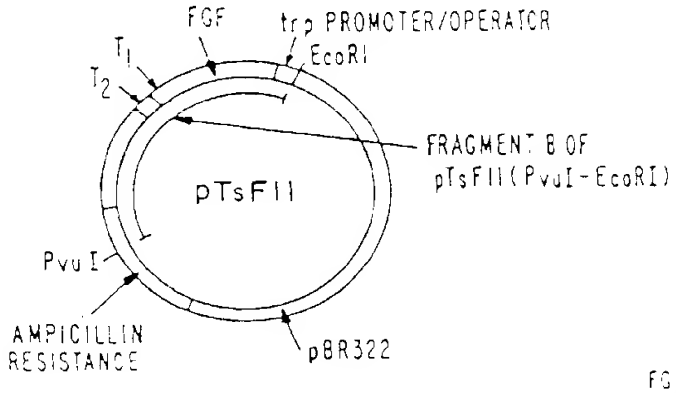
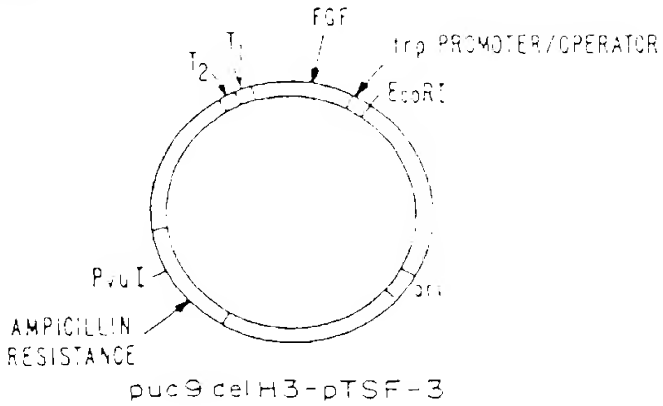

FGF
trp PROMOTER/OPERATOR
T1
T2
EcoRI
FRAGMENT B OF pTsF11(PvuI-EcoRI)
pTsF11
PvuI
AMPICILLIN RESISTANCE
pBR322

FIG. 5


FGF
T1
T2
trp PROMOTER/OPERATOR
EcoRI
PvuI
AMPICILLIN RESISTANCE
puc9delH3-pTSF-3

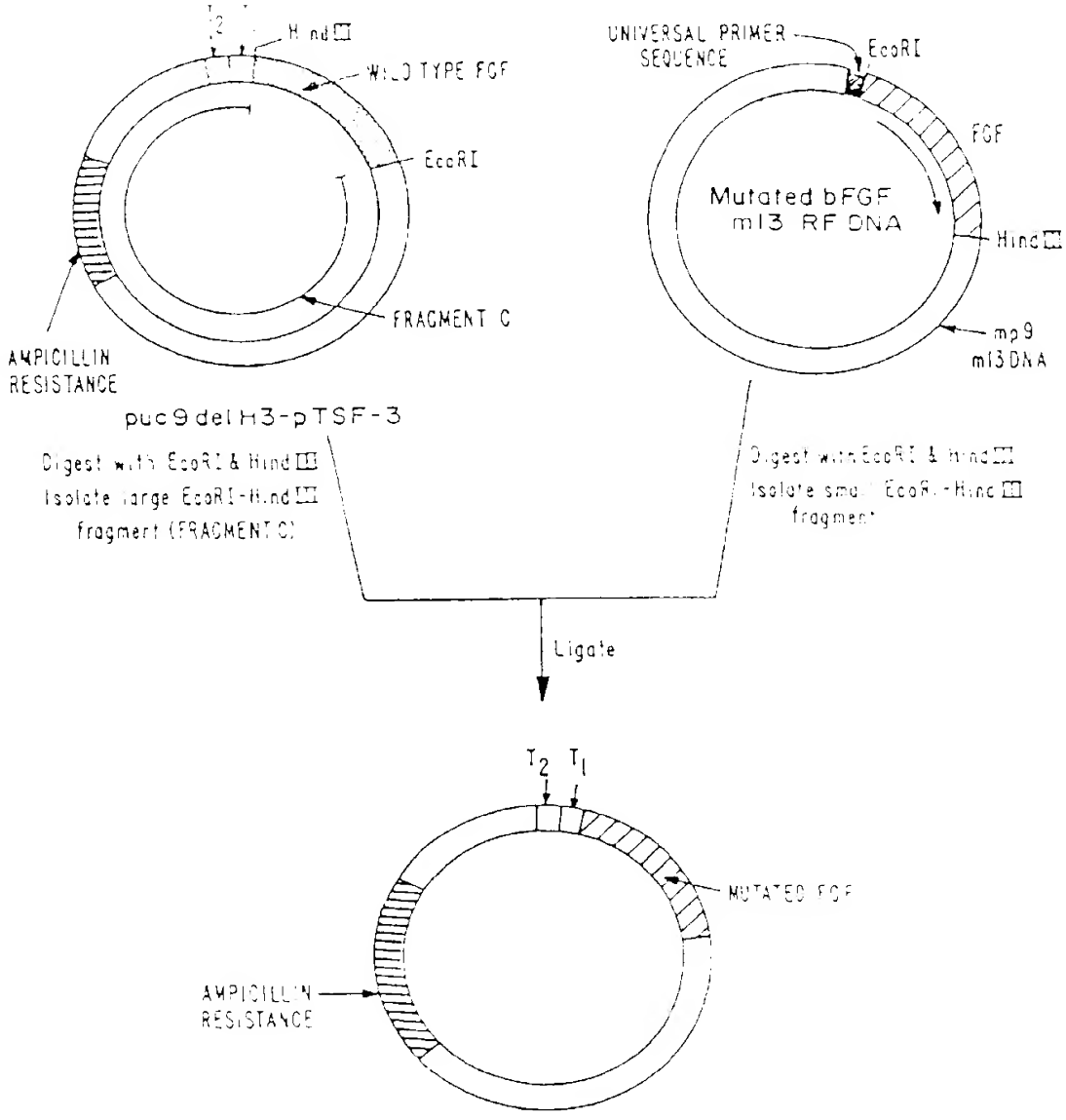

T2
T1
Hind III
WILD TYPE FGF
EcoRI
FRAGMENT C
AMPICILLIN RESISTANCE
puc9 del H3-pTSF-3
Digest with EcoRI & Hind III
Isolate large EcoRI-Hind III fragment (FRAGMENT C)
UNIVERSAL PRIMER SEQUENCE
EcoRI
FGF
Mutated bFGF m13 RF DNA
Hind III
mp9 m13 DNA
Digest with EcoRI & Hind III
Isolate small EcoRI-Hind III fragment
Ligate
T2
T1
MUTATED FGF
AMPICILLIN RESISTANCE

FIG. 6

FIG. 7